

60
 1 ATGTGGAATGGATACTGACACATTGTGCCTCAGCCTTTCCCCACCTGCCCCGGCTGCTGC
 -----+-----+-----+-----+-----+-----+-----+
 TACACCTTTACCTATGACTGTGTAACACGGAGTCGGAAGGGGTGGACGGGCCGACGACG
 -----+-----+-----+-----+-----+-----+-----+
M W K W I L L T H C A S A F P H L P G C C C
 61 TGCTGCTGCTTTTGTGTGTTCTTGGTGCTTCCGTCCTGTCACCTGCCAAGCCCTT
 -----+-----+-----+-----+-----+-----+-----+
 ACGACGACGAAAAACAACGACAAGAACCACAGAAGGCAGGGACAGTGGACGGTTCGGGAA
 -----+-----+-----+-----+-----+-----+-----+
C C C F L L L F L V S S V P V I C Q A L
 121 GGTGAGGACATGGTGTACCCAGAGGCCACCAACTTCTTCCCTCCCTCTCCTCTCCT
 -----+-----+-----+-----+-----+-----+-----+
 CCAGTCCTGTACCACAGTGGTCTCCGGTGTGAGAAAGAGGAGGAGGAGGAGGAGGA
 -----+-----+-----+-----+-----+-----+-----+
 G Q D M V S P E A T N S S S S S S S P
 181 TCCAGCGCGGGAAGGCATGTGCGGAGCTACAATCACCTTCAAGGAGATGTCGCGTGGAGA
 -----+-----+-----+-----+-----+-----+-----+
 AGGTCGCGCCCTTCCGTACACGCCTCGATGTTAGTGAAGTTCTCTACAGGCGACCTCT
 -----+-----+-----+-----+-----+-----+-----+
 S S A G R H V R S Y N H L Q G D V R W R

FIG. 1A

MATCH WITH FIG.1A

241 AAGCTATTCCTTTACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGTCAGCGGG
 -----+-----+-----+-----+-----+-----+-----+
 TTCGATAAGAGAAAGTGGTTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC 300

K L F S F T K Y F L K I E K N G K V S G

301 ACCAAGAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAAATCGGAGTT
 -----+-----+-----+-----+-----+-----+-----+
 TGGTTCTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA 360

T K K E N C P Y S I L E I T S V E I G V

361 GTTGCCGTCAAAGCCATTAAACAGCAACTATTACTTAGCCATGAACAAGAGGGGAACTC
 -----+-----+-----+-----+-----+-----+-----+
 CAACGGCAGTTTCGGIAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCTTTGAG 420

V A V K A I N S N Y Y L A M N K K G K L

421 TATGGCTCAAAAGAAATTTAACAATGACTGTAGCTGAAGGAGAGGATAGAGGAAAAATGGA
 -----+-----+-----+-----+-----+-----+-----+
 ATACCGAGTTTCTTAAATGTTACTGACATTCGACTTCCTCTCCTATCCTTTTACCT 480

Y G S K E F N N D C K L K E R I E E N G

MATCH WITH FIG.1C

FIG.1B

481 -----+-----+-----+-----+-----+-----
ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATAACCGTAAC

Y N T Y A S F N W Q H N G R Q M Y V A L

AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAAACACGAAGAAAAAACACCTCTGCTCAC
600 -----+-----+-----+-----+-----+-----
TTACCTTTTCTCGAGGTTCCCTCCTCCTGCTCTTTTGCTTCCCTTTTGTGGAGACGAGTG

N G K G A P R R G Q K T R R K N T S A H

TTTTCTTCCAATGGTGGTACACTCATAG
601 -----+-----+-----+-----+-----
AAAGAAGGTTACCAACCATGTGAGTATC
F L P M V V H S *

Fig. 10

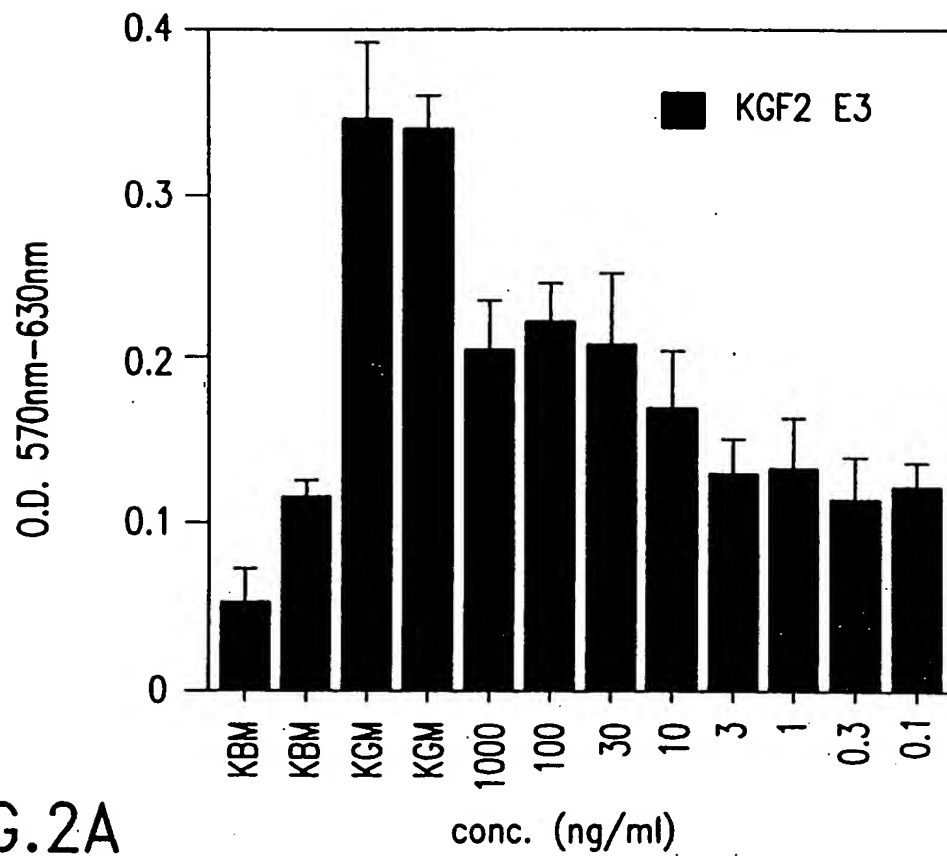


FIG.2A

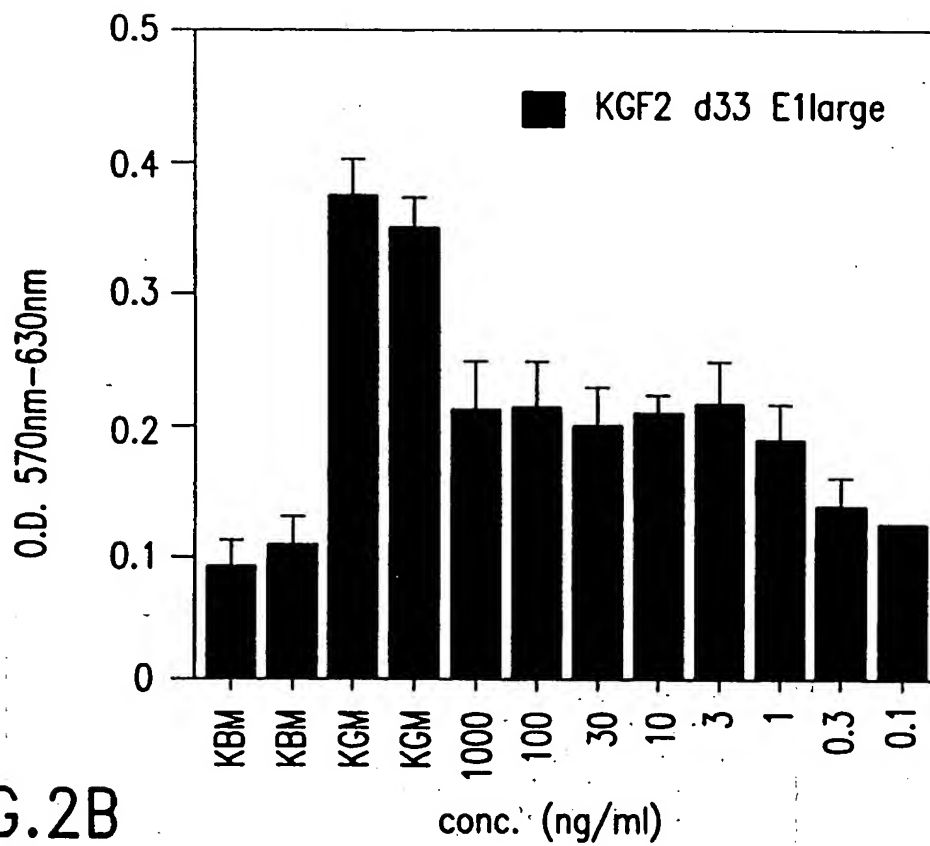


FIG.2B

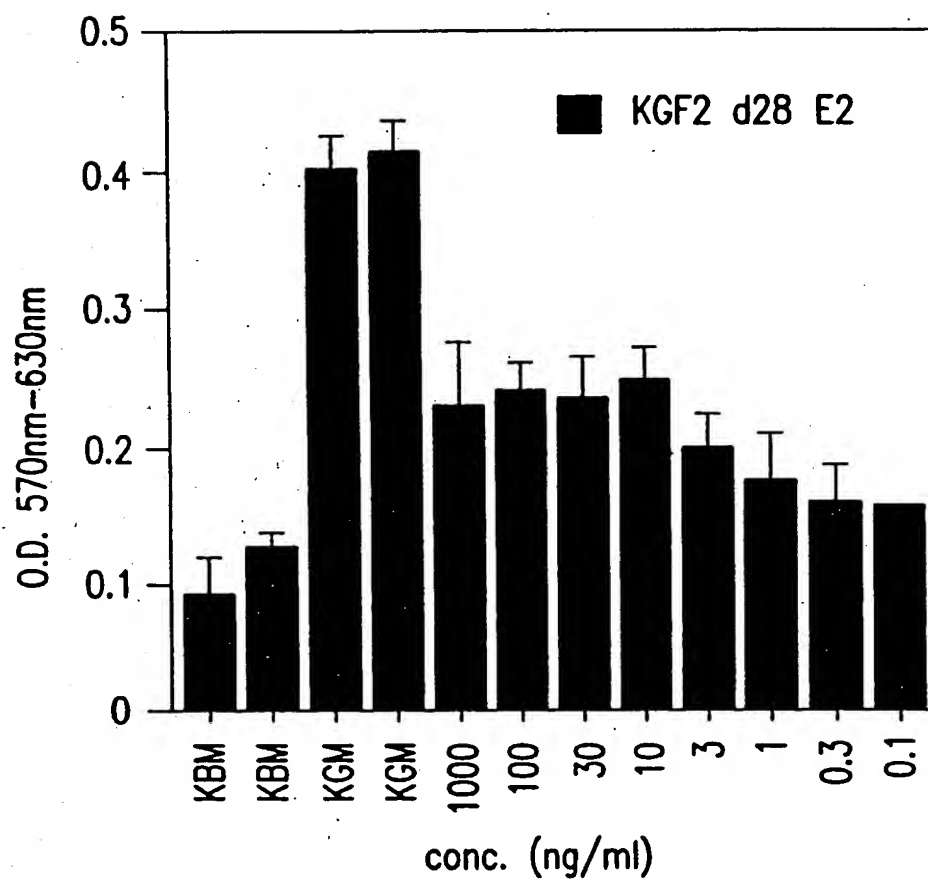


FIG.2C

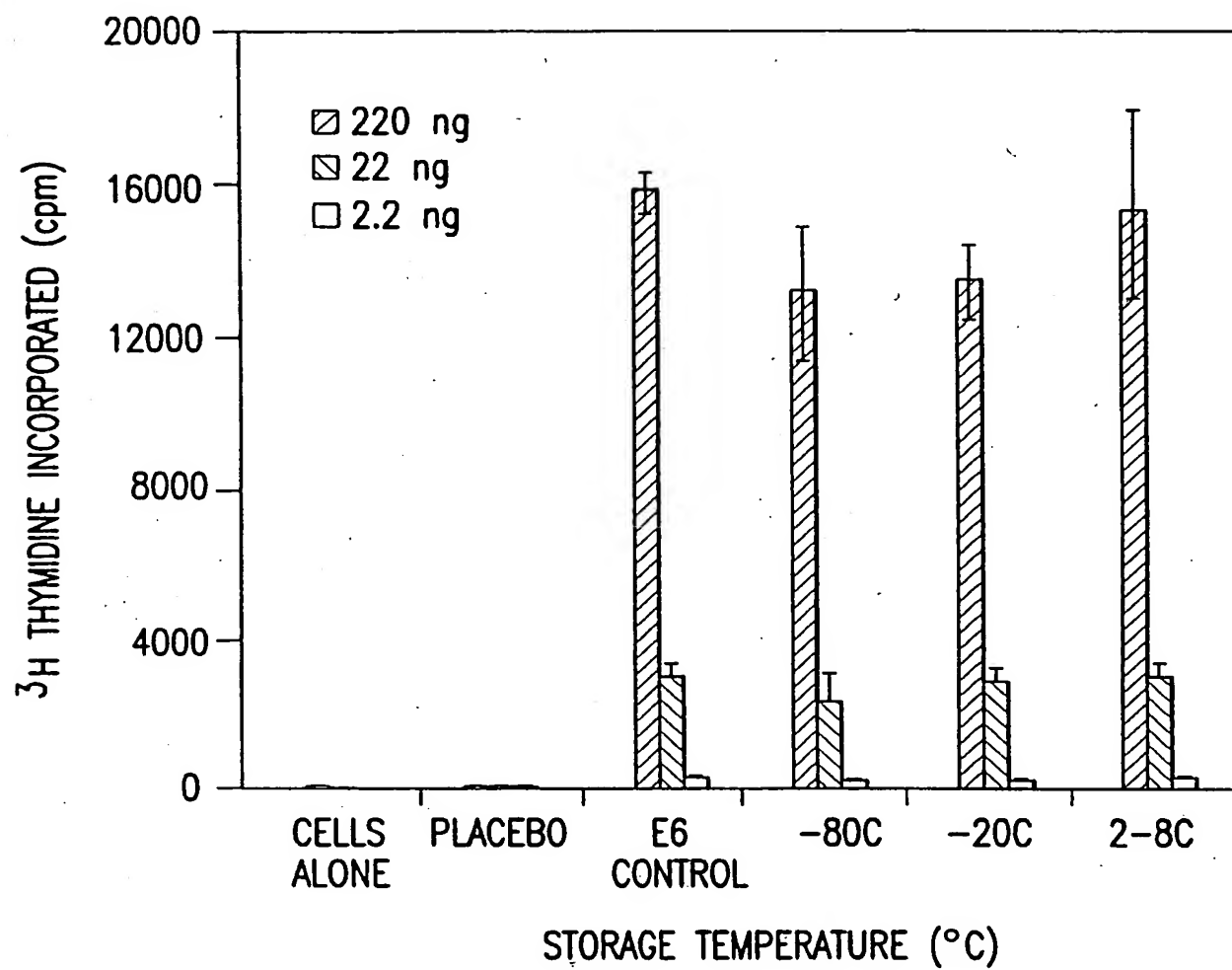


FIG.3

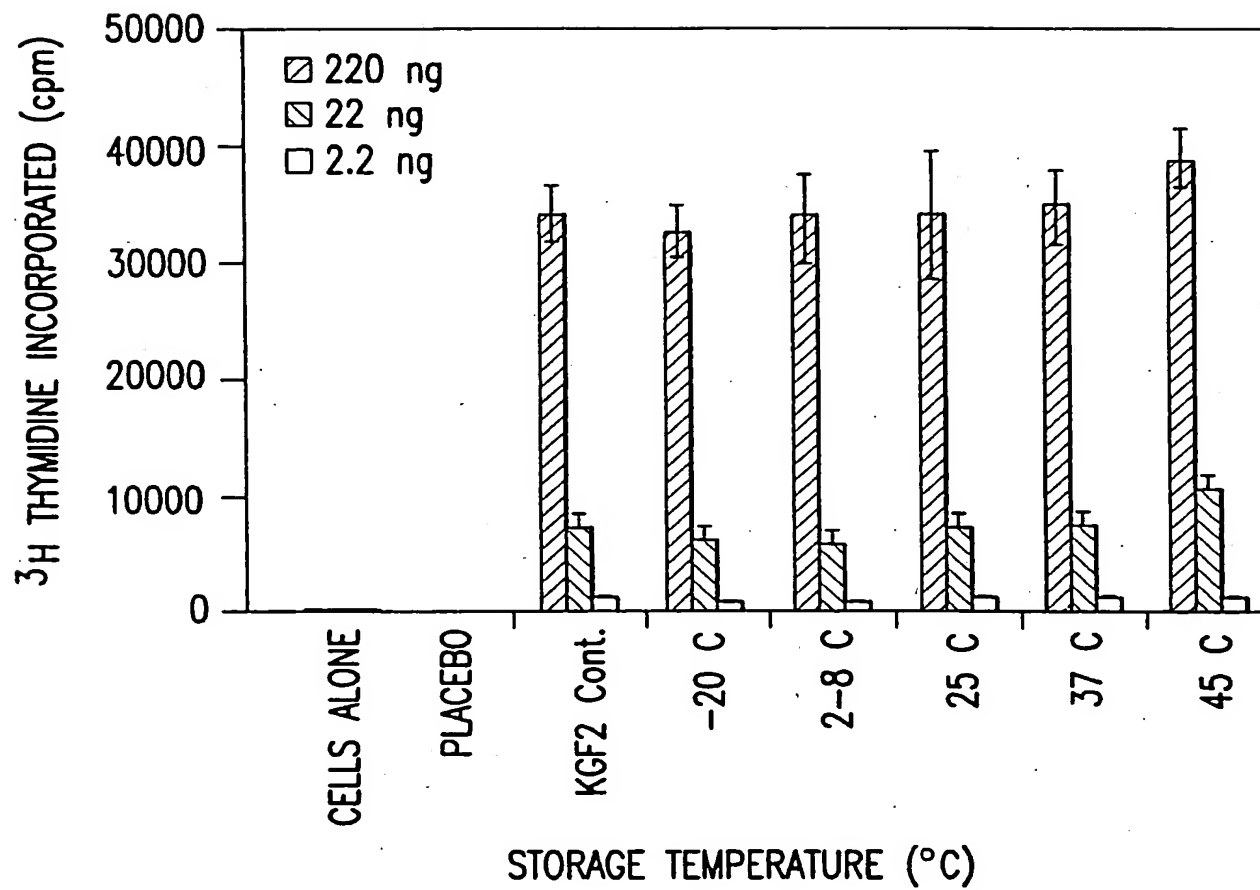


FIG.4

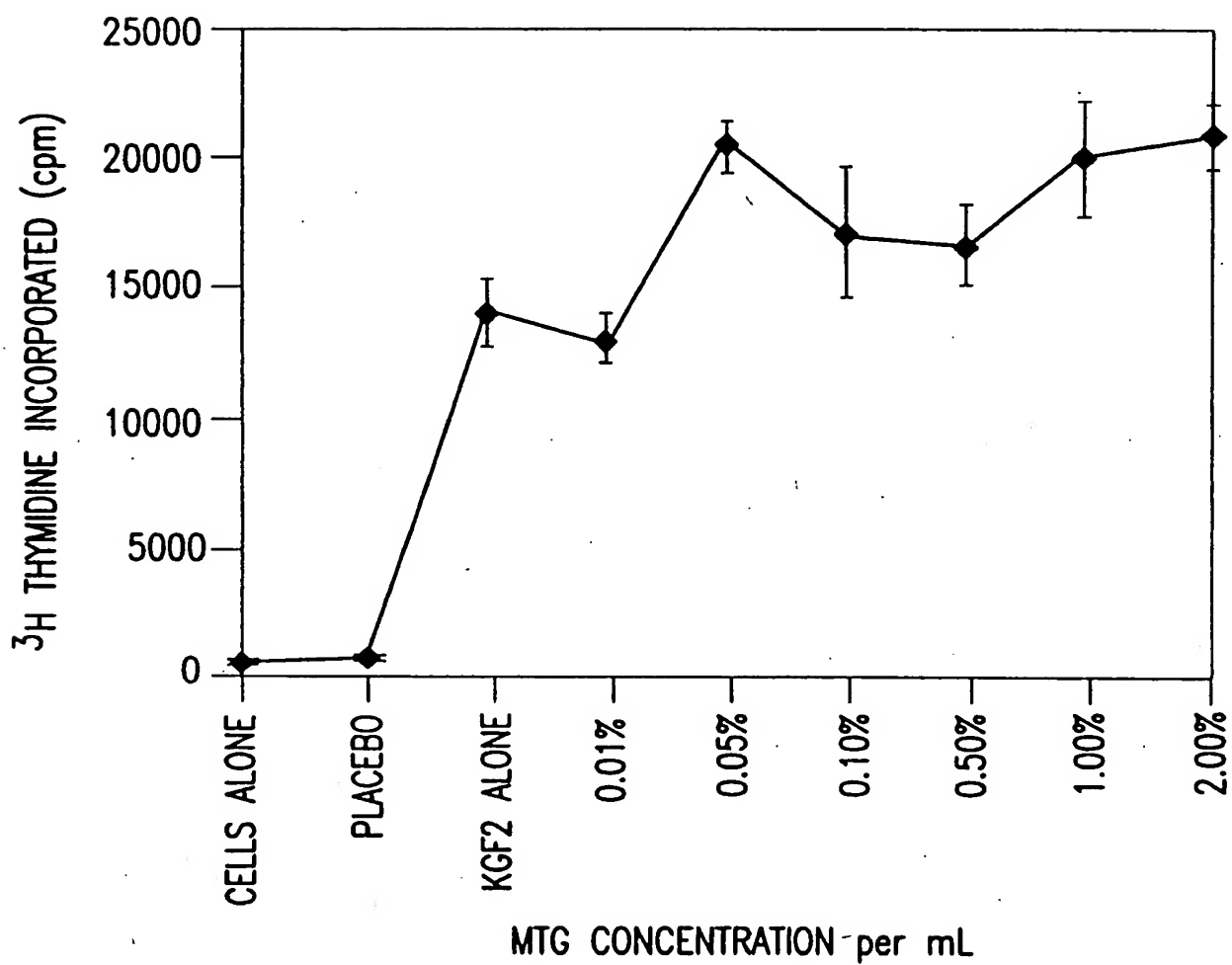


FIG.5